

GenCore version 5.1.4_p5_4578
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Score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model		Result No.				Description			
		Score	Query Match	Length	DB ID				
Run on:	March 11, 2003, 11:21:13 ; Search time 9051 Seconds (without alignments) 17430.815 Million cell updates/sec	c 1	34.6	0.6	50 6 AR178318	AR178318 Sequence			
Title:	US-10-006-911-3	c 2	34.6	0.6	50 6 AX323400	AX323400 Sequence			
Perfect score:	5421	c 3	30.6	0.6	31 6 AX248013	AX248013 Sequence			
Sequence:	1 cccggatccgggttttttg. tgtttcaaaaaaaaaaa 5421	c 4	30.6	0.6	31 6 AX248014	AX248014 Sequence			
Scoring table:	IDENTITY_NUC	c 5	30.4	0.6	49 6 AX099434	AX099434 Sequence			
Searched:	Gapext 10_0 , Gapext 1.0	c 6	29.8	0.5	44 6 I31473	I31473 Sequence			
Total number of hits satisfying chosen parameters:	841850	c 7	28.2	0.5	43 6 AX484406	AX484406 Sequence			
Minimum DB seq length:	0	c 8	28	0.5	45 6 E50989	E50989 Method for			
Maximum DB seq length:	50	c 9	27.8	0.5	40 6 A48799	A48799 Sequence			
Post-processing:	Minimum Match 0%	c 10	27.8	0.5	43 6 AX225198	AX225198 Sequence			
	Maximum Match 100% Listing first 1000 summaries	c 11	27.8	0.5	44 6 AR038858	AR038858 Sequence			
		c 12	27.8	0.5	50 6 AX261361	AX261361 Sequence			
		c 13	27.8	0.5	50 6 I36502	I36502 Sequence			
		c 14	27.4	0.5	50 6 AX164808	AX164808 Sequence			
		c 15	27.2	0.5	46 6 AX287579	AX287579 Sequence			
		c 16	27.2	0.5	46 6 AX287583	AX287583 Sequence			
		c 17	26.8	0.5	30 6 AR208348	AR208348 Sequence			
		c 18	26.8	0.5	38 6 AX207477	AX207477 Sequence			
		c 19	26.4	0.5	37 6 AX106972	AX106972 Sequence			
		c 20	26.4	0.5	37 6 I29931	I29931 Sequence			
		c 21	26.4	0.5	38 6 E50766	E50766 Vector expr			
		c 22	26.4	0.5	46 6 AX287581	AX287581 Sequence			
		c 23	26.4	0.5	48 6 AX166869	AX166869 Sequence			
		c 24	26.4	0.5	49 3 DDU63607	DDU63607 Dictyosteli			
		c 25	26.2	0.5	41 6 I29926	I29926 Sequence			
		c 26	26.2	0.5	44 6 I29927	I29927 Sequence			
		c 27	26.2	0.5	50 6 I23510	I23510 Sequence			
		c 28	26.2	0.5	50 6 I28359	I28359 Sequence			
		c 29	26.2	0.5	50 6 I28514	I28514 Sequence			
		c 30	26.2	0.5	50 6 I41125	I41125 Sequence			
		c 31	26.2	0.5	50 6 I49056	I49056 Sequence			
		c 32	26.2	0.5	50 6 I70295	I70295 Sequence			
		c 33	26.2	0.5	50 6 I90068	I90068 Sequence			
		c 34	26	0.5	47 6 AX458031	AX458031 Sequence			
		c 35	26	0.5	50 6 AX158154	AX158154 Sequence			
		c 36	25.8	0.5	50 6 AX287571	AX287571 Sequence			
		c 37	25.8	0.5	50 6 AX287575	AX287575 Sequence			
		c 38	25.6	0.5	42 6 I32405	I32405 Sequence			
		c 39	25.6	0.5	46 6 AX287577	AX287577 Sequence			
		c 40	25.6	0.5	50 6 I23510	I23510 Sequence			
		c 41	25.6	0.5	50 6 I28359	I28359 Sequence			
		c 42	25.6	0.5	50 6 I28514	I28514 Sequence			
		c 43	25.6	0.5	50 6 I41125	I41125 Sequence			
		c 44	25.6	0.5	50 6 I49056	I49056 Sequence			
		c 45	25.6	0.5	50 6 I7C295	I7C295 Sequence			
		c 46	25.6	0.5	50 6 I90068	I90068 Sequence			
		c 47	25.4	0.5	37 6 I29925	I29925 Sequence			
		c 48	25.4	0.5	41 6 A62423	A62423 Sequence			
		c 49	25.4	0.5	43 6 AR071826	AR071826 Sequence			
		c 50	25.4	0.5	43 6 AR112566	AR112566 Sequence			
		c 51	25.4	0.5	47 6 AX378317	AX378317 Sequence			
		c 52	25.4	0.5	47 12 SYNPRWA	M94403 Artificial			
		c 53	25.4	0.5	50 6 AX001307	AX001307 Sequence			
		c 54	25.4	0.5	50 6 AX441077	AX441077 Sequence			
		c 55	25.4	0.5	50 6 E36243	E36243 Human semap			
		c 56	25.4	0.5	50 6 AX206861	AX206861 Sequence			
		c 57	25.2	0.5	44 6 AX441076	AX441076 Sequence			
		c 58	25.2	0.5	47 6 AX441077	AX441077 Sequence			
		c 59	25.2	0.5	48 6 AX441076	AX441076 Sequence			
		c 60	25.2	0.5	50 6 AX158154	AX158154 Sequence			
		c 61	25	0.5	37 9 HSOBRI05	HSOBRI05 Human QPR g			
		c 62	25	0.5	45 6 E50989	E50989 Method for			
		c 63	24.8	0.5	28 6 AR208346	AR208346 Sequence			
		c 64	24.8	0.5	29 6 AR098648	AR098648 Sequence			
Pred. No.	is the number of results predicted by chance to have a	65	24.8	0.5	29 6 AF204722	AF204722 Sequence			

66	24	8	0.5	4.3	€	AX395321	Sequence	
67	24	8	0.5	4.3	€	AX443022	Sequence	
68	24	8	0.5	4.3	€	AX459616	Sequence	
C	69	24	8	0.5	4.6	€	AX287578	Sequence
C	70	24	8	0.5	4.6	€	AX287582	Sequence
71	24	6	0.5	4.4	€	AP039858	Sequence	
72	24	6	0.5	4.5	€	AR001540	Sequence	
73	24	6	0.5	4.8	€	AR020989	Sequence	
74	24	6	0.5	4.8	€	AP043404	Sequence	
75	24	6	0.5	4.8	€	AP062319	Sequence	
76	24	6	0.5	4.8	€	AR193778	Sequence	
77	24	4	0.5	3.0	€	AX079109	Sequence	
78	24	4	0.5	3.5	€	AP029830	Sequence	
C	79	24	4	0.5	3.6	€	I299920	Sequence 43
B0	80	24	4	0.5	4.3	€	I78646	Sequence 1
C	81	24	4	0.5	4.5	€	AX287571	Sequence
C	82	24	4	0.5	4.5	€	AX287575	Sequence
C	83	24	4	0.5	4.6	€	AX287578	Sequence
C	84	24	4	0.5	4.6	€	AX287582	Sequence
85	24	4	0.5	4.6	€	I45570	Sequence 5	
C	86	24	4	0.5	5.0	€	AX157157	Sequence
C	87	24	2	0.4	3.2	€	AR022289	Sequence
C	88	24	2	0.4	3.2	€	AP053140	Sequence
89	24	2	0.4	3.3	€	AP099615	Sequence	
an	24	2	0.4	3.7	€	AP120128	Sequence	
91	24	2	0.4	3.7	€	I29931	Sequence 44	
C	92	24	2	0.4	3.8	€	E50766	Vector expr
C	93	24	2	0.4	4.5	€	AP202973	Sequence
C	94	24	2	0.4	4.5	€	AX172348	Sequence
C	95	24	2	0.4	4.5	€	AY287569	Sequence
C	96	24	2	0.4	4.5	€	AX287573	Sequence
C	97	24	2	0.4	4.7	€	AP078060	Sequence
C	98	24	0.4	2.4	2.6	€	AP098647	Sequence
C	99	24	0.4	2.4	2.6	€	AP204721	Sequence
C	100	24	0.4	2.4	3.1	€	BD011883	Detection
C	101	24	0.4	2.4	3.3	2.3	BD004363	Detection
C	102	24	0.4	2.4	3.8	5	AY009603	Sequence
C	103	24	0.4	4.2	6	AP020971	Sequence	
C	104	24	0.4	4.2	6	AP043386	Sequence	
C	105	24	0.4	4.2	6	AP062301	Sequence	
C	106	24	0.4	4.2	6	AP183760	Sequence	
C	107	24	0.4	4.2	6	AX287570	Sequence	
C	108	24	0.4	4.2	6	AX287574	Sequence	
C	109	24	0.4	4.2	6	AX320946	Sequence	
C	110	24	0.4	4.2	6	AX320847	Sequence	
C	111	24	0.4	4.2	6	AX175242	Sequence	
C	112	24	0.4	4.6	6	AY287579	Sequence	
C	113	24	0.4	4.6	6	AY287583	Sequence	
C	114	24	0.4	4.6	6	AY320846	Sequence	
C	115	23	0.4	4.6	6	AY175242	Sequence	
C	116	23	0.4	4.6	6	AX052989	Sequence	
C	117	23	0.4	4.6	6	A63565	Sequence 6	
C	118	23	0.4	4.6	6	AX158156	Sequence	
C	119	23	0.4	4.6	6	AX164809	Sequence	
C	120	23	0.4	4.6	6	AR001551	Sequence	
C	121	23	0.4	4.6	6	AR001550	Sequence	
C	122	23	0.4	4.6	6	AP001549	Sequence	
C	123	23	0.4	4.6	6	AP001548	Sequence	
C	124	23	0.4	4.6	6	AP001547	Sequence	
C	125	23	0.4	4.6	6	AP071842	Sequence	
C	126	23	0.4	4.6	6	AP112582	Sequence	
C	127	23	0.4	4.6	6	AP003731	Sequence	
C	128	23	0.4	4.6	6	AP010067	Sequence	
C	129	23	0.4	4.6	6	AP055273	Sequence	
C	130	23	0.4	4.6	6	AP141202	Sequence	
C	131	23	0.4	4.6	6	AR141439	Sequence	
C	132	23	0.4	4.6	6	I11911	Sequence 21	
C	133	23	0.4	4.6	6	I40484	Sequence 21	
C	134	23	0.4	4.6	6	AX458031	Sequence	
C	135	23	0.4	4.6	6	AR128993	Sequence	
C	136	23	0.4	4.6	6	AR128994	Sequence	
C	137	23	0.4	4.6	6	AX458031	Sequence	
138	23	0.4	4.6	4.7	6	AP128995	Sequence	

4.3	23.8	0.4	4.9	6	AX441075	Sequence	
4.3	23.8	0.4	5.0	6	AX187454	Sequence	
4.3	23.6	0.4	5.0	6	AF082115	Sequence	
4.6	23.6	0.4	5.0	6	AX164808	Sequence	
C	140	23.6	0.4	5.0	6	AR174581	Sequence
C	141	23.6	0.4	5.0	6	AX106717	Sequence
C	142	23.6	0.4	5.0	6	I79494	Sequence 1
C	143	23.4	0.4	5.0	6	I79494	H. sapiens
C	144	23.4	0.4	5.0	6	AP08914	(
C	145	23.4	0.4	5.0	6	AX43022	Sequence
C	146	23.4	0.4	5.0	6	AX459616	Sequence
C	147	23.4	0.4	5.0	6	AF029615	Sequence
C	148	23.4	0.4	5.0	6	AP126128	Sequence
C	149	23.4	0.4	5.0	6	I29924	Sequence 37
C	150	23.4	0.4	5.0	6	AX395321	Sequence
C	151	23.4	0.4	5.0	6	AX443022	Sequence
C	152	23.4	0.4	5.0	6	AX459616	Sequence
C	153	23.4	0.4	5.0	6	AX459616	Sequence
C	154	23.4	0.4	5.0	6	AX28647	Sequence 2
C	155	23.4	0.4	5.0	6	I78649	Sequence 4
C	156	23.4	0.4	5.0	6	I78651	Sequence 6
C	157	23.4	0.4	5.0	6	I78656	Sequence 11
C	158	23.4	0.4	5.0	6	AY206861	Sequence
C	159	23.4	0.4	5.0	6	AR003731	Sequence
C	160	23.4	0.4	5.0	6	AR010067	Sequence
C	161	23.4	0.4	5.0	6	AP055273	Sequence
C	162	23.4	0.4	5.0	6	AR141202	Sequence
C	163	23.4	0.4	5.0	6	AR141439	Sequence
C	164	23.4	0.4	5.0	6	I11911	Sequence 21
C	165	23.4	0.4	5.0	6	I40484	Sequence 21
C	166	23.4	0.4	5.0	6	AY194782	Sequence
C	167	23.4	0.4	5.0	6	AY133326	Sequence
C	168	23.4	0.4	5.0	6	AR082114	Sequence
C	169	23.4	0.4	5.0	6	AX157852	Sequence
C	170	23.2	0.4	5.0	6	AP162080	Sequence
C							

C 212	23	0.4	24	6	AR128996	Sequence 2
C 213	23	0.4	24	6	AR202467	Sequence 2
C 214	23	0.4	24	6	AR2C2468	Sequence 2
C 215	23	0.4	24	6	AR2C2469	Sequence 2
C 216	23	0.4	24	6	AR2C2470	Sequence 2
C 217	23	0.4	24	6	AR2C2471	Sequence 2
C 218	23	0.4	24	6	AR2C2472	Sequence 2
C 219	23	0.4	24	6	BD011883	Detection
C 220	23	0.4	23	3	BD004363	Detection
C 221	23	0.4	24	6	A63578	Sequence 19
C 222	23	0.4	24	6	AF071746	Sequence 19
C 223	23	0.4	35	6	I35032	Sequence 11
C 224	23	0.4	35	6	AX009604	Sequence 4
C 225	23	0.4	34	6	AX009605	Sequence 4
C 226	23	0.4	35	6	AF071758	Sequence 4
C 227	23	0.4	35	6	A49109	Sequence 4
C 228	23	0.4	42	6	AX287570	Sequence 4
C 229	23	0.4	45	6	AX287574	Sequence 4
C 230	23	0.4	45	6	AX287574	Sequence 4
C 231	23	0.4	47	6	AX114342	Sequence 4
C 232	23	0.4	48	6	AR020989	Sequence 4
C 233	23	0.4	48	6	ARC43404	Sequence 4
C 234	23	0.4	48	6	ARC62319	Sequence 4
C 235	23	0.4	48	6	AR071849	Sequence 4
C 236	23	0.4	48	6	AR112589	Sequence 4
C 237	23	0.4	48	6	AP183778	Sequence 4
C 238	23	0.4	48	9	S64862S2	alpha 1-the
C 239	23	0.4	50	6	AX160956	Sequence 7
C 240	22	0.4	47	6	M24990	S. cerevisiae
C 241	22	0.4	33	6	I45569	Sequence 4
C 242	22	0.4	35	6	AR001553	Sequence 4
C 243	22	0.4	36	6	ARC36355	Sequence 4
C 244	22	0.4	36	6	I12572	Sequence 18
C 245	22	0.4	37	2	U62489	Human OBR 3
C 246	22	0.4	41	6	AX320844	Sequence 3
C 247	22	0.4	43	6	I78648	Sequence 3
C 248	22	0.4	43	6	I78650	Sequence 5
C 249	22	0.4	43	6	I78652	Sequence 7
C 250	22	0.4	43	6	I78657	Sequence 12
C 251	22	0.4	48	6	AX05227C2	Sequence 27
C 252	21	0.4	49	11	G73668	RZ220R etio
C 253	22	0.4	50	6	AX156806	Sequence 10
C 254	22	0.4	50	6	AX187454	Sequence 10
C 255	22	0.4	50	6	AX2C4524	Sequence 10
C 256	22	0.4	27	6	AX327980	Sequence 10
C 257	22	0.4	30	6	AR051244	Sequence 10
C 258	22	0.4	30	6	AR127791	Sequence 10
C 259	22	0.4	30	6	I28373	Sequence 12
C 260	22	0.4	32	6	AX430213	Sequence 12
C 261	22	0.4	40	5	A43785	Sequence 10
C 262	22	0.4	40	6	I84451	Sequence 10
C 263	22	0.4	42	6	AR148431	Sequence 10
C 264	22	0.4	47	6	AR078060	Sequence 10
C 265	22	0.4	47	6	AX114342	Sequence 10
C 266	22	0.4	50	6	AR082114	Sequence 10
C 267	22	0.4	50	6	ARC82116	Sequence 10
C 268	22	0.4	50	6	ARC86862	Sequence 10
C 269	22	0.4	24	6	AR010037	Sequence 10
C 270	22	0.4	24	6	AR034772	Sequence 10
C 271	22	0.4	24	6	AR202876	Sequence 10
C 272	22	0.4	24	6	AR068465	Sequence 10
C 273	22	0.4	24	6	AR105984	Sequence 10
C 274	22	0.4	24	6	AR167972	Sequence 10
C 275	22	0.4	24	6	AR104770	Sequence 10
C 276	22	0.4	24	6	AR104771	Sequence 10
C 277	22	0.4	24	6	AX104769	Sequence 10
C 278	22	0.4	24	6	AX184443	Sequence 10
C 279	22	0.4	24	6	AX354553	Sequence 10
C 280	22	0.4	24	6	AX355813	Sequence 10
C 281	22	0.4	24	6	AX427163	Sequence 10
C 282	22	0.4	24	6	AX428574	Sequence 10
C 283	22	0.4	24	6	I24762	Sequence 10
C 284	22	0.4	25	6	AP105982	Sequence 10
				3	HSPFL2	Sequence 10
				3	AF068857	Human Sapi

358	2.2	6	AX104716	21.8	C	431	50	6	I47698
359	2.2	6	AX418162	21.8	C	432	50	6	I7312C
C 360	2.2	6	AX418163	21.6	C	433	24	6	AX391871
C 361	2.2	0.4	3.0	6	A43784	Sequence 9	0.4	3.0	AR001542
C 362	2.2	0.4	3.0	6	A62991	Sequence 3	0.4	3.0	AR084537
C 363	2.2	0.4	3.0	6	A62995	Sequence 7	0.4	3.0	AR064078
C 364	2.2	0.4	3.0	6	AR179066	Sequence	0.4	3.0	BD008477
C 365	2.2	0.4	3.0	6	AR179070	Sequence	0.4	3.0	AX299729
C 366	2.2	0.4	3.0	6	AX104902	Sequence	0.4	3.0	AP064077
C 367	2.2	0.4	3.0	6	AX104903	Sequence	0.4	3.0	AX009469
C 368	2.2	0.4	3.0	6	AX474673	Sequence	0.4	3.0	AX320846
C 369	2.2	0.4	3.0	6	AX474674	Sequence	0.4	3.0	AX320847
C 370	2.2	0.4	3.0	6	E04638	Synthesized	0.4	3.0	BD008476
C 371	2.2	0.4	3.0	6	E04684	Synthetic n	0.4	3.0	I32116 Sequence 6
C 372	2.2	0.4	3.0	6	I84450	Sequence 9	0.4	3.0	I32121 Sequence 11
C 373	2.2	0.4	3.5	6	AP019230	Sequence	0.4	3.5	AR019243 Sequence
C 374	2.2	0.4	3.5	6	AP019252	Sequence	0.4	3.5	AR112589 Sequence
C 375	2.2	0.4	3.5	6	AP036353	Sequence?	0.4	3.5	AP162086 Sequence
C 376	2.2	0.4	3.6	6	AP084536	Sequence	0.4	3.6	AP166611 Sequence
C 377	2.2	0.4	3.6	6	112570	Sequence 16	0.4	3.6	AX160478 Sequence
C 378	2.2	0.4	3.6	6	172101	Sequence 16	0.4	3.6	AX161079 Sequence
C 379	2.2	0.4	3.6	6	182050	Sequence 89	0.4	3.6	AX162044 Sequence
C 380	2.2	0.4	4.0	6	AY299738	Sequence	0.4	4.0	AX394507 Sequence
C 381	2.2	0.4	4.2	6	A79693	Sequence 27	0.4	4.2	AX394514 Sequence
C 382	2.2	0.4	4.2	6	AX050342	Sequence	0.4	4.2	AX052989 Sequence
C 383	2.2	0.4	4.5	6	AR002600	Sequence	0.4	4.5	AX080522 Sequence
C 384	2.2	0.4	4.9	1.1	G73668	RZZ2CR etio	0.4	4.5	I29922 Sequence 35
C 385	2.2	0.4	5.0	6	AX157140	Sequence	0.4	5.0	E07882 PCR primer
C 386	2.2	0.4	5.0	6	AY164948	Sequence	0.4	5.0	I35C32 Sequence 11
C 387	21.8	0.4	25	6	AX116188	Sequence	0.4	25	AX465470 Sequence
C 388	21.8	0.4	26	6	AP098647	Sequence	0.4	26	A59198 Sequence 7
C 389	21.8	0.4	26	6	AP204721	Sequence	0.4	26	A93431 Sequence 4
C 390	21.8	0.4	29	6	APn98648	Sequence	0.4	29	AP079191 Sequence
C 391	21.8	0.4	29	6	AP204722	Sequence	0.4	29	AR149881 Sequence
C 392	21.8	0.4	3.4	6	AR001554	Sequence	0.4	3.4	AX001999 Sequence
C 393	21.8	0.4	3.5	6	AR029831	Sequence	0.4	3.5	AX235336 Sequence
C 394	21.8	0.4	3.6	6	AY009600	Sequence	0.4	3.6	AX299737 Sequence
C 395	21.8	0.4	4.0	6	AP016506	Sequence?	0.4	4.0	AX361592 Sequence
C 396	21.8	0.4	4.0	6	AP096889	Sequence	0.4	4.0	AX484472 Sequence
C 397	21.8	0.4	4.0	6	AY299729	Sequence	0.4	4.0	I78653 Sequence 8
C 398	21.8	0.4	4.0	6	AY299730	Sequence	0.4	4.0	I78658 Sequence 13
C 399	21.8	0.4	4.0	6	AY299737	Sequence	0.4	4.0	A32899 Synthetic t
C 400	21.8	0.4	4.1	6	AP204722	Sequence	0.4	4.1	AX361592 Sequence
C 401	21.8	0.4	4.1	6	AY320845	Sequence	0.4	4.1	AX287569 Sequence
C 402	21.8	0.4	4.2	6	AY299729	Sequence	0.4	4.2	AX287573 Sequence
C 403	21.8	0.4	4.5	6	AY304972	Sequence	0.4	4.5	E21691 Spermatozen
C 404	21.8	0.4	4.5	6	AX306501	Sequence	0.4	4.5	AX417660 Sequence
C 405	21.8	0.4	4.5	6	I32114	Sequence 4	0.4	4.5	AX45980 Sequence
C 406	21.8	0.4	4.6	6	A65286	Sequence 9	0.4	4.6	AX209894 Sequence
C 407	21.8	0.4	4.6	6	AR116106	Sequence	0.4	4.6	AX356068 Sequence
C 408	21.8	0.4	4.6	6	AR150434	Sequence	0.4	4.6	AX417660 Sequence
C 409	21.8	0.4	4.6	6	AR179887	Sequence	0.4	4.6	AX279697 Sequence
C 410	21.8	0.4	4.7	6	AX009261	Sequence	0.4	4.7	AX161079 Sequence
C 411	21.8	0.4	4.8	6	A65285	Sequence 8	0.4	4.8	AX164963 Sequence
C 412	21.8	0.4	4.9	6	AP150433	Sequence	0.4	4.9	AX164964 Sequence
C 413	21.8	0.4	4.9	6	AR172420	Sequence	0.4	4.9	AX174582 Sequence
C 414	21.8	0.4	4.9	6	AP093198	Sequence	0.4	4.9	AX351711 Sequence
C 415	21.8	0.4	4.9	6	AP093198	Sequence	0.4	4.9	AN0914 H sapiens (
C 416	21.8	0.4	4.9	6	AY160080	Sequence?	0.4	4.9	AP174572 Sequence
C 417	21.8	0.4	4.9	6	AY160490	Sequence	0.4	4.9	AX179588 Sequence
C 418	21.8	0.4	5.0	6	AP4756	Sequence	0.4	5.0	AP110113 Sequence
C 419	21.8	0.4	5.0	6	AP050168	Sequence	0.4	5.0	AX350101 Sequence
C 420	21.8	0.4	5.0	6	AR072090	Sequence	0.4	5.0	AX355814 Sequence
C 421	21.8	0.4	5.0	6	AP093198	Sequence	0.4	5.0	E04985 DNA sequence
C 422	21.8	0.4	5.0	6	AP104719	Sequence	0.4	5.0	AX427136 Sequence
C 423	21.8	0.4	5.0	6	AP123332	Sequence	0.4	5.0	AX351712 Sequence
C 424	21.8	0.4	5.0	6	AX157184	Sequence	0.4	5.0	AX351711 Sequence
C 425	21.8	0.4	5.0	6	AX160080	Sequence	0.4	5.0	AN0914 H sapiens (
C 426	21.8	0.4	5.0	6	AY160490	Sequence?	0.4	5.0	AP174572 Sequence
C 427	21.8	0.4	5.0	6	E11533	Linker-primer	0.4	5.0	AX179588 Sequence
C 428	21.8	0.4	5.0	6	E15768	Cleicnucleo	0.4	5.0	AP110113 Sequence
C 429	21.8	0.4	5.0	6	E30813	Novel prote	0.4	5.0	114300 Sequence 1
C 430	21.8	0.4	5.0	6	E54866	Process for	0.4	5.0	I29226 Sequence 3.

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C	521	21	0.4	34	6	A23805	Artificial
C	522	21	0.4	36	6	AX13627	Sequence 12
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C	531	21	0.4	41	6	E16035	DNA primer
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C 802	20	0.4	50	6	I36503	Sequence I36503 Sequence	C 875 19.8	0.4	48	14	MMLTRA3
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C 812	19.8	0.4	30	6	AX196237	Sequence AX196237 Sequence	C 885 19.8	0.4	50	6	AX159100
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C 835	19.8	0.4	35	6	AP172572	Sequence AP172572 Sequence	C 908 19.6	0.4	42	6	AR158212
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C 839	19.8	0.4	35	6	AR071839	Sequence AR071839 Sequence	C 912 19.6	0.4	48	6	AR016736
C 840	19.8	0.4	35	6	A25167	Sequence A25167 Oligonucleo	C 913 19.6	0.4	48	6	AR016737
C 841	19.8	0.4	35	6	AP0056789	Sequence AP0056789 Sequence	C 914 19.6	0.4	48	6	AP070602
C 842	19.8	0.4	35	6	AR164652	Sequence AR164652 Sequence	C 915 19.6	0.4	48	6	AR079463
C 843	19.8	0.4	35	6	AP028999	Sequence AP028999 Sequence	C 916 19.5	0.4	48	6	AX441070
C 844	19.8	0.4	36	6	I96229	Sequence I96229 Sequence 12	C 917 19.6	0.4	48	6	AR441076
C 845	19.8	0.4	37	6	A25167	Sequence A25167 Synthetic B	C 918 19.6	0.4	48	6	189764
C 846	19.8	0.4	38	6	AR164652	Sequence AR164652 Sequence	C 919 19.6	0.4	49	6	AX441067
C 847	19.8	0.4	38	6	AP028999	Sequence AP028999 Sequence	C 920 19.6	0.4	49	6	X75470
C 848	19.8	0.4	39	6	AR065937	Sequence AR065937 Sequence	C 921 19.6	0.4	50	3	DMDPDHP3
C 849	19.8	0.4	40	6	A25350	Sequence A25350 Synthetic B	C 922 19.6	0.4	50	6	AP024001
C 850	19.8	0.4	41	6	AR135397	Sequence AR135397 Sequence	C 923 19.6	0.4	50	6	AR211829
C 851	19.8	0.4	41	6	AR019476	Sequence AR019476 Sequence	C 924 19.6	0.4	50	6	AX156809
C 852	19.8	0.4	42	6	AR184440	Sequence AR184440 Sequence	C 925 19.6	0.4	50	6	AX156811
C 853	19.8	0.4	42	6	AP184441	Sequence AP184441 Sequence	C 926 19.6	0.4	50	6	AX158106
C 854	19.8	0.4	43	6	AR354550	Sequence AR354550 Sequence	C 927 19.6	0.4	50	6	AX158108
C 855	19.8	0.4	43	6	AX354551	Sequence AR354551 Sequence	C 928 19.6	0.4	50	6	AX158568
C 856	19.8	0.4	43	6	AX428578	Sequence AX428578 Sequence	C 929 19.6	0.4	50	6	AX161960
C 857	19.8	0.4	44	6	AX483525	Sequence AX483525 Sequence	C 930 19.6	0.4	50	6	AX164811
C 858	19.8	0.4	45	6	AX484406	Sequence AX484406 Sequence	C 931 19.6	0.4	50	6	AX164907
C 859	19.8	0.4	45	6	E12626	Sequence E12626 Sequence	C 9				

ACCESSION E50989
VERSION E50989.1 GI:18622166
KEYWORDS JP 2000000267-A/3
SOURCE synthetic construct.

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 45)
AUTHORS Fujimura,K.
TITLE Method for measuring nucleic acid and kit therefor
JOURNAL Patent. JF 200000267 A 3 31 OCT 2000;
GIJITSU PREPYI KIMIAI TECNICO FISICO YKII YENYI SHC
COMMENT OS Artificial Sequence
PN JP 2000300267-A/3
PD 31-OCT-2000
PF 21-APR-1999 JP 1999113165
PR
KATSUYA FUJIMURA
CN15/0971251/EP, P12N1c/00
PC
CC
FH Key Location/Qualifiers
FT source 1..45 /organism="Artificial Sequence"
FT Location/Qualifiers
FEATURES source 1..45 /organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 40 a 4 c 1 g 0 t
ORIGIN

Query Match 0.5%; Score 27.8; DB 6; Length 43;
Best Local Similarity 82.1%; Pred. No. 2.9e+05;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
JOURNAL
FEATURES source 1..43 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic DNA"
BASE COUNT 43 a 0 c 0 g 43 t
ORIGIN

Query Match 0.5%; Score 27.8; DB 6; Length 43;
Best Local Similarity 82.1%; Pred. No. 2.9e+05;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
JOURNAL
FEATURES source 1..43 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic DNA"
BASE COUNT 43 a 0 c 0 g 43 t
ORIGIN

RESULT 11
AP038858/c
LOCUS AP038858
DEFINITION Sequence 9 from patent US 5807703.
ACCESSION AP038858
VERSION AP038858 1
KEYWORDS GJ-5958221
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Jacobs,F., McCoy,J.M., Lavallie,E.P., Racine,L.A., Martiny,R.,
Treacy,M., Evans,C., Spaulding,V. and Bowman,M.
TITLE Secreted Proteins and Polymyocutides encoding them
JOURNAL Patent. US 5807703-A 9 15-SEP-1998;
FEATURES source 1..44 /organism="unknown"
BASE COUNT 43 a 0 c 0 g 0 t
ORIGIN

Query Match 0.5%; Score 27.8; DB 6; Length 44;
Best Local Similarity 82.1%; Pred. No. 2.9e+05;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
JOURNAL
FEATURES source 1..44 /organism="unknown"
/db_xref="taxon:32630"
/note="synthetic DNA"
BASE COUNT 43 a 0 c 0 g 0 t
ORIGIN

RESULT 12
AX261361
LOCUS AX261361
DEFINITION Sequence 1012 from Patent WO170277.
ACCESSION AX261361
VERSION AX261361.1 GI:16510328
KEYWORDS SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Meagher,M.J., Xie,J. and King,G.E.
TITLE Compositions and methods for therapy and diagnostics of colon cancer

Query Match 0.5%; Score 27.8; DB 6; Length 43;
Best Local Similarity 82.1%; Pred. No. 2.9e+05;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
JOURNAL
FEATURES source 1..43 /organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 40 a 0 c 0 g 0 t
ORIGIN

Query Match 0.5%; Score 27.8; DB 6; Length 43;
Best Local Similarity 82.1%; Pred. No. 2.9e+05;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
JOURNAL
FEATURES source 1..43 /organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 40 a 0 c 0 g 0 t
ORIGIN

RESULT 10
AX225198
LOCUS AX225198

JOURNAL Patent: WO 0173027-A 1012 04-OCT-2001;
 CORIXA CORPORATION (US)
 Location/Qualifiers
 1. .50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

FEATURES source
 BASE COUNT 0 a 0 c 0 g 50 t
 ORIGIN

Query Match Best Local Similarity 82.1%; Pred. No. 2.9e+05;
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3117 TTCTTTCTCCTCCCTTTTTTGTGTTT 3155
 Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTT 39

RESULT 13
 I36502/C LOCUS I36502 Sequence 1 from patent US 5607834.
 DEFINITION I36502
 VERSION I36502.1 GI:2086327
 KEYWORDS Unknown
 SOURCE Unknown
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Bagwell,C.Bruce.
 TITLE Fluorescent imperfect hairpin nucleic acid probes
 JOURNAL Patent : US 5607834-A 1 04-MAR-1997;
 FEATURES source
 BASE COUNT 50 a 0 c 0 g 0 t
 ORIGIN

Query Match Best Local Similarity 82.1%; Pred. No. 2.9e+05;
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3117 TTCTTTCTCCTCCCTTTTTTGTGTTT 3155
 Db 50 TTTTTTTTTTTTTTTTTTTTTTTT 12

RESULT 14
 AX164808 LOCUS AX164808 Sequence 3 from Patent WO0138586.
 DEFINITION AX164808
 VERSION AX164808.1 GI:14545637
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Shimkets,R.A. and Leach,M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent : WO 0138586-A 3 31-MAY-2001;
 Curagen Corporation (US)
 FEATURES source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 misc_feature 25..26
 /note="Nucleotide deleted between bases 25 and 26
 Accession number cg43314087"
 variation 26
 /note="single nucleotide polymorphism"

BASE COUNT 7 a 2 c 12 g 29 t
 ORIGIN

Query Match 0.5%; Score 27.4; DB 6; Length 50;
 Best Local Similarity 75.6%; Pred. No. 3.6e+05;
 Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 4875 TTTTGTTGGTTGTTATTGTTAAAGGTTAAATTGCACT 4919
 Db 6 TTTTTTGGTTTGTGTTTGTGTTTAAGGCAAAGGGTCT 50

RESULT 15
 AX287579 LOCUS AX287579 Sequence 22 from Patent WO0177390.
 DEFINITION AX287579
 ACCESSION AX287579.1 GI:17049345
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 VERSION 1
 AUTHORS abarz,A.P.
 TITLE Process for allele discrimination utilizing primer extension
 JOURNAL Patent : WO 0177390-A 22 18-OCT-2001;
 Molecular Staging, Inc. (US)

FEATURES source
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="P1 primer for use in allele discrimination"

BASE COUNT 2 a 3 c 0 g 41 t
 ORIGIN

Query Match 0.5%; Score 27.2; DB 6; Length 46;
 Best Local Similarity 80.0%; Pred. No. 4e+05;
 Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3117 TTCTTTCTCCTCCCTCCTTTTTTTTTTTTTTTA 3156
 Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTCTA 40

RESULT 16
 AX287583 LOCUS AX287583 Sequence 26 from Patent WO0177390.
 DEFINITION AX287583
 ACCESSION AX287583.1 GI:17049349
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 VERSION 1
 AUTHORS abarz,A.P.
 TITLE Process for allele discrimination utilizing primer extension
 JOURNAL Patent : WO 0177390-A 26 18-OCT-2001;
 Molecular Staging, Inc. (US)

FEATURES source
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="P1 primer for use in allele discrimination"

BASE COUNT 1 a 3 c 0 g 42 t
 ORIGIN

Query Match 0.5%; Score 27.2; DB 6; Length 46;
 Best Local Similarity 80.0%; Pred. No. 4e+05;
 Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3117 TTCTTTCTCCTCCCTTCTTTTTTTTTTTTTTTA 3156

OS	Artificial Sequence	Nucleic acid amplification and detection of mycobacterium species
PN	JP 2000152793-A/19	Patent. WO 0144510-A 35 21-JUN-2001;
PD	06-JUN-2000	Gen-probe Incorporated (US) ; Biomerieux S.A. (FR)
PF	24-JUN-1999 JP 1999178347	Location/Qualifiers
PR	MICHINORI OBARA, KYOKO OBARA, KAZUNARI TABIRA, JUNICHI MATSUZAKI,	1. .48
PI	HIROSHI OMORI	/organism="synthetic construct"
PI	C12N15/09, A01K67/C07, C12N5/10, C12Q1/70, C12N15/00, C12N5/00 CC	/db_xref="taxon:32630"
PC		/note="Capture Oligomer"
FH	Key	modified_base
FT	source	modified_base /mod_base=cm.
FEATURES	source	modified_base /note="2' -O-methoxy-thymidine"
FT	source	modified_base /mod_base=OTHER
FEATURES	source	modified_base /note="2' -O-methoxy-adenosine"
FT	source	modified_base /mod_base=OTHER
FEATURES	source	modified_base /note="2' -O-methoxy-thymidine"
FT	source	modified_base /mod_base=OTHER
FEATURES	source	modified_base /note="2' -O-methoxy-adenosine"
BASE COUNT	ORIGIN	1 a 2 c 0 g 35 t
ORIGIN	Query Match	0.5%; Score 26.4; DB 6; Length 38;
ORIGIN	Best Local Similarity	83.3%; Pred. No. 5.9e+05;
ORIGIN	Matches	30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy	3119	CTTTCTCCTCCCTTTTGTGTTTTTT 3154
Db	3	CTTTTTTTTTTTTTTTTTTTTTTT 38
RESULT 22	AX287581	Query Match 0.5%; Score 26.4; DB 6; Length 48;
LOCUS	Sequence 24 from Patent WO0177390.	Best Local Similarity 75.0%; Pred No. 6e+05;
DEFINITION	AX287581	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0
ACCESSION	AX287581.1	Accession 3128 TTCCTTTTTTTTTAAGAGCCTGTGATAGT 3171
VERSION	GI:17049347	Version U63607
KEYWORDS	.	Version U63607.1 GI:2393760
SOURCE	abarr A, P.	Source Dictyostelium discoideum.
ORGANISM	Process for allele discrimination utilizing primer extension	Organism Eukaryota; Dictyosteliida; Dictyostelium.
REFERENCE	1.46	Author Wells, D.J.
AUTHORS	Patent: WO 0177390-A 24 18-OCT-2001;	Title Tdd-4, a DNA transposon of Dictyostelium similar to LTR retroelement integrases
TITLE	Molecular Staging, Inc. (US)	Journal Nuclieic Acids Res. 27 (11), 2408-2415 (1999)
JOURNAL	Location/Qualifiers	Medline 99263047
FEATURES	source	Query Match 0.5%; Score 26.4; DB 6; Length 46;
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Result 24 DDU63607
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Locus DDU63607
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Definition Dictyostelium discoideum Tdd-4 transposable element flanking sequence, clone p435 left end.
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Accession U63607
BASE COUNT	ORIGIN	Score 26.4; DB 6; Length 46;
ORIGIN	7 a 4 c 0 g 35 t	Keywords Wells, D.J.
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Reference 1 (bases 1 to 49)
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Authors Wells, D.J.
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Title Tdd-4, a DNA transposon of Dictyostelium similar to LTR retroelement integrases
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Journal Nuclieic Acids Res. 27 (11), 2408-2415 (1999)
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Medline 10325432
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Pubmed 2 (bases 1 to 49)
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Authors Wells, D.J. and Welker, D.L.
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Reference 1 (bases 1 to 48)
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Authors Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodriguez, M.
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Title Tdd-4, a DNA transposon of Dictyostelium similar to LTR retroelement integrases
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Journal Nuclieic Acids Res. 27 (11), 2408-2415 (1999)
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Medline 99263047
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Authors Wells, D.J. and Welker, D.L.
BASE COUNT	ORIGIN	Best Local Similarity 75.0%; Pred. No. 6e+05;
ORIGIN	7 a 4 c 0 g 35 t	Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Reference 1 (bases 1 to 48)
ORIGIN	Query Match 0.5%; Score 26.4; DB 6; Length 46;	Authors Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodriguez, M.

JOURNAL Patent: US 5587443-A 2 24-DEC-1996;
 FEATURES Location/Qualifiers
 source 1. .42
 /organism="unknown"
 BASE COUNT 2 a 4 c 2 g 34 t
 ORIGIN

Query Match 0.5%; Score 25.6; DB 6; Length 42;
 Best Local Similarity 77.5%; Pred. No. 9e+05;
 Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS abarz, A., P.
 TITLE Process for allele discrimination utilizing primer extension
 JOURNAL Patent: WO 017390-A 20 18-OCT 2001;
 Molecular Staging, Inc. (US)
 FEATURES Location/Qualifiers
 source 1. .46
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="P1 primer for use in allele discrimination"
 BASE COUNT 8 a 4 c 0 g 34 t
 ORIGIN

Query Match 0.5%; Score 25.6; DB 6; Length 46;
 Best Local Similarity 77.5%; Pred. No. 9e+05;
 Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Baker, J., Chien, K., King, K., Pennice, D. and Wood, W.
 TITLE Cardiac hypertrophy factor and uses therefor
 JOURNAL Patent: US 5534615-A 5 09-JUL-1996;
 FEATURES Location/Qualifiers
 source 1. .50
 /organism="unknown"
 BASE COUNT 3 a 7 c 7 g 33 t
 ORIGIN

Query Match 0.5%; Score 25.6; DB 6; Length 50;
 Best Local Similarity 87.5%; Pred. No. 9.1e+05;
 Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 KEYWORD

